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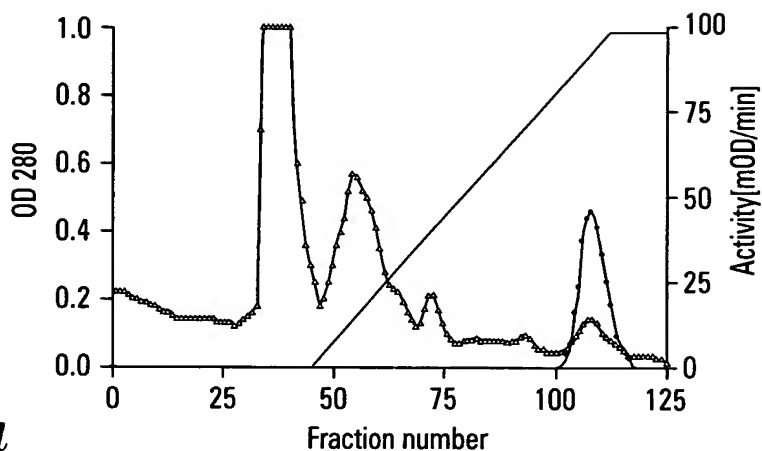


Fig. 1a

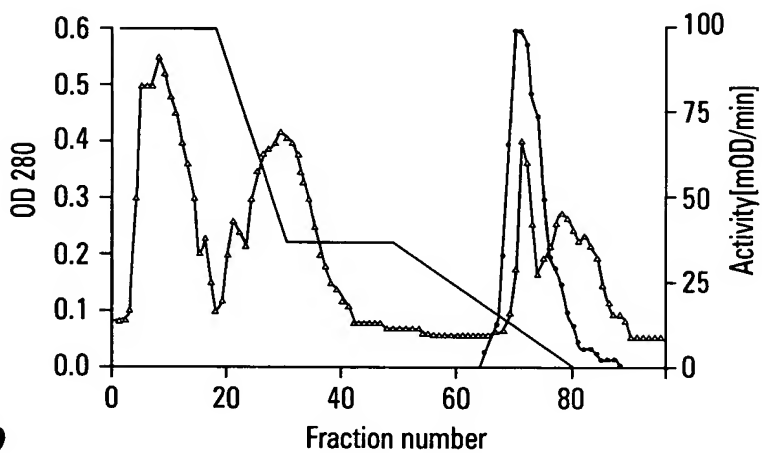


Fig. 1b

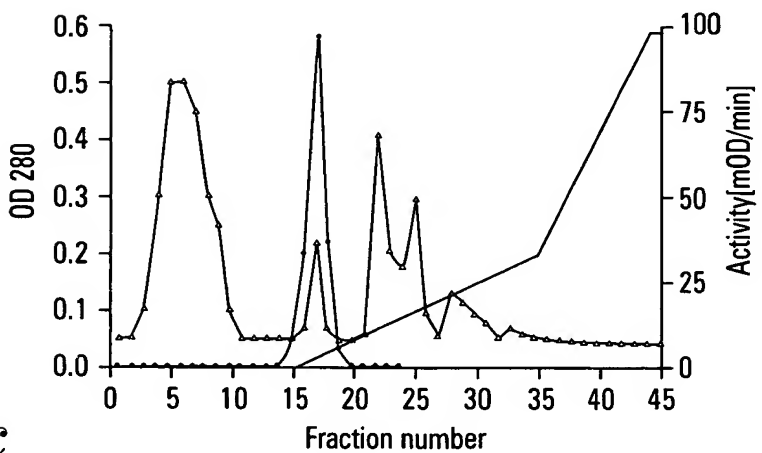


Fig. 1c

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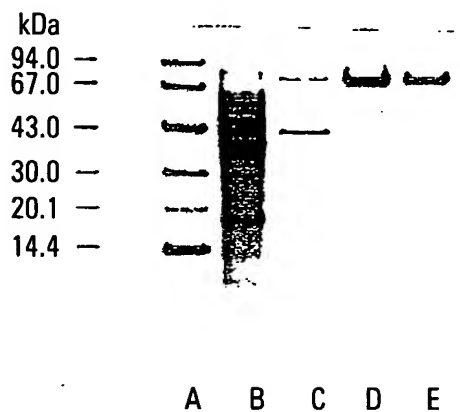


Fig. 2

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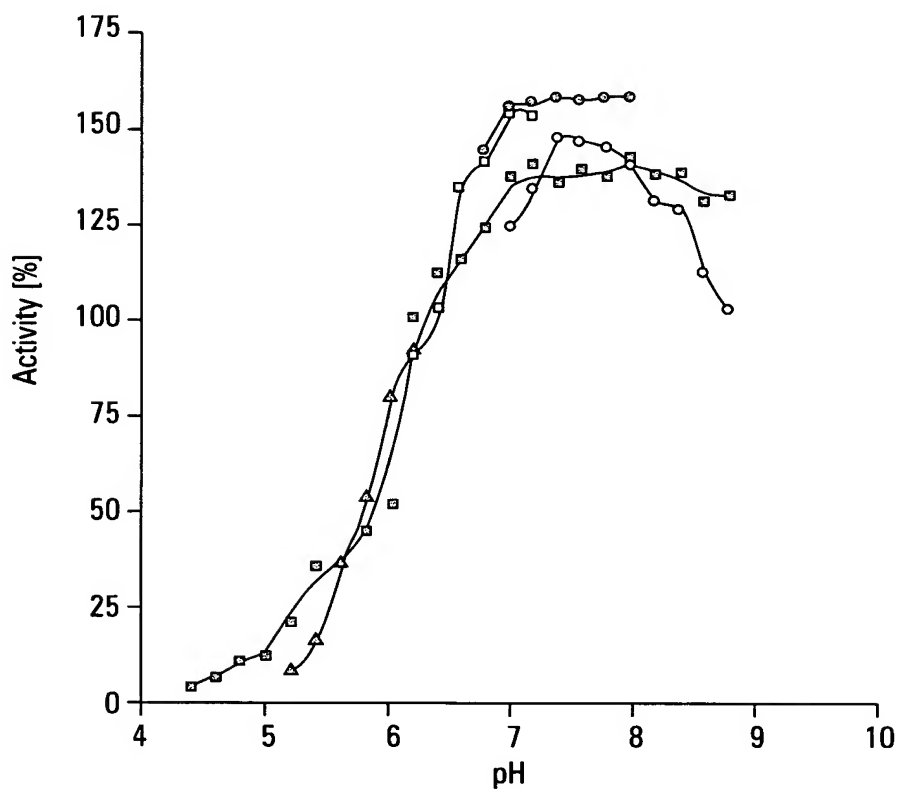


Fig. 3

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Fig. 4a

Fig. 4b

Fig. 4

Fig. 4a

SEQ ID NO:1 atgcaaatgaaataaaagtattcttctcggagcagccctgctgttggtgcttcagggttagccaaagccgacaaagcagcatgtggctc 90
SEQ ID NO:2 M Q M K L K S I L L G A A L L L G A S G V A K A D K G M W L 30

ctcaacgaactcaatcaggagaaatctggatcgatgcgtgagctcggttttacgctcccggttggttcgctctacagtttcgacaaagccg 180
L N E L N Q E N L D R M R E L G F T L P L D S L Y S F D K P 60

tccattgccaatgccgtggtttatcttcggtggcggtatccggtatcacagtgtccggtcagggcctgatctttaccacaccaccactgc 270
S I A N A V V I F G G C T G I T V S D Q G L I F T N H H C 90

ggatacgggtgctatccagagccaaagcacggtggatcacgactatctgcgcgatggttttcgcttctcgcacgatgggtgagggagcttc 360
G Y G A I Q S Q S T V D H D Y L R D G F V S R T M G E E L P 120

attccgggtctttccgtgaagtatctgcgcaagatcgtgaaggtaacggacaaggtagaaggacagctcaagggtatcactgacgagatg 450
I P G L S V K Y L R K I V K V T D K V E G Q L K G I T D E M 150

gagcgtctgcgcaagctcaggaggtatgccaaagaactggccaaaaaataatgcagacgagaaacaaactctgcctcgtagagccttc 540
E R L R K A Q E V C Q E L A K E N A D E N Q L C I V E P F 180

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Y S N N E Y F L I V Y D V F K D V R M V F A P S S V G K F 210

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gaatacagcaaggacaaataaacccctataaagcccggttacttcgctgcgtatccatgcaagggtacaaggctgacgactatgccatgacc 810
E Y S K D N K P Y K P V Y F A A V S M Q G Y K A D D Y A M T 270

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I G F P G S T D R Y L T S W G V E D R I E N E N P R I E V 300

cgcggtatcaagcaaggcatctggaagggaagccatgagcgcagatcaggctaccggtatcaaatatgccagcaagtatgctcagagtgc 990
R G I K Q G I W K E A M S A D Q A T R I K Y A S K Y A Q S A 330

aactattggaagaattcggtatgaaccgggtctcgtcgtcttgacgtgataggtcgtaagcgtgcgaggaagagcattcgca 1080
N Y W K N S I G M N R G L A R L D V I G R K R A E E R A F A 360





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Fig. 4b

gactggatccgtaagaacggcaagagtgtgtctatggcgatgtattgtcttctctcgaaggcttataaggaagagagccaagggccaac 1170
D W I R K N G K S A V Y G D V L S S L E K A Y K E G A K A N 390
cgtgagatgacttatttgagcgagacgctcttcggtgtaccgaggtgtgtgttttgcacagtttgcacacgcatgtggctacaaaatcct 1260
R E M T Y L S E T L F G G T E V V R F A Q F A N A L A T N P 420
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D A H A G I L K S L D D K Y K D Y L P S L D R K V L P A M L 450
gatattgtacgccgggtatccctgccgacaagctccccgatattcaagaatgtaatcgacaagaaattcaaggcgacacgaagaag 1440
D I V R R I P A D K L P D I F K N V I D K K F K G D T K K 480
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Y A D F V F D K S V V P Y S D K F H A M L K S M D K E K F A 510
aaggctatcgagaaagatccggcagtagagctttcccaagagcgtaatagtctgctcgctatttcagggccgatggccaatgcc 1620
K A I E K D P A V E L S K S V I A A A R A I Q A D A M A N A 540
tatgccattgagaagggaagcgtcttttcttccggttttcgctgagatgtaccccgacgtgctctgcccagcgatgcccaacttcacc 1710
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aagcaggatccctaagagcgatgagtttgcgtacagagagaataatcctcgacctcttccgcaccaaactatggtcgctatgccgagaac 1890
K Q D P K S D E F A V Q E N I L D L F R T K N Y G R Y A E N 630
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G Q L H I A F L S N N D I T G G N S G S P V F D K N G R L I 660
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G L A F D G N W E A M S G D I E F E P D L Q R T I S V D I R 690
tacgttcttctcatgattgacaaaatggggtcagtgcccccgctctcatccaaagagctgaagttgatctaa 2139
Y V L F M I D K W G Q C P R L I Q E L K L I *



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SEQ ID No: 3	DPP-7	644	TGNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRYVLFM	695
			TGNSGSPV++ +IG+ + G +G + + + + +I + F	
SEQ ID No: 4	V-8	704	TGNSGSPVFNEKNEVIGIHWGGVPNEFNGAVFINENVRNFLKQNIEDIHFA	863

Fig. 5

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Fig. 6a

Fig. 6b

Fig. 6

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SEQ ID NO: 5	S1	1	MASQALGFLHONGLNTMKKWLISVAASAFASHADEGMMQPHOLP-AMADVLKAKGLEIDAKSISKLETFPMN--AVTSE
SEQ ID NO: 6	S2	1	-----MRITAAALVLTCTGATADEGMMQPYQMP-SIADKLSARGIDIPADKLEADLTSYPMN--AVVGL
SEQ ID NO: 7	X	1	-----MRFNLISLSVLAITLITVDSITHAGEGMMVPOQLP-ETAGPLKQAGLQLSPEQLSNLTGDPMG--AVVSL
SEQ ID NO: 8	P1	1	-----MQMKLKSITLGAALILGASGVAKADKGMWLLNELNQENLDRMRELGFITPLDLSVYSFDPKPSITANAVVIFG
SEQ ID NO: 9	P2	1	-----MKKRLLLPFLAVMLCLCOIAHADEGMMWLMQQLG-RKYAQMKERGLKMKKEYDLYNPNGTSLKDAVWLF
	S1	78	GGCTASFVSPKGLVVTNHHCAVCSIQVNSIPKNNLQDGFIAKTFADLPAAPGSRVYVITEDVINVTERVKAGLENKGTG-
	S2	62	GYCTASFVSPQGLVVTNHHCAVKAIOVNTKKEHNYLEQGFRLATSMCKEPSAGPNERLYITTEAVHDTVISDMTKDISQDP--
	X	66	GNCSTASVSPKGLVVTNHHCAVGAIOVNSTPKNNLIKKEGFNALTOADEVSAGPNARIVYEQITDVTIAQAKAALAAAGND
	P1	71	GGCTGITVSDQGLIFVTNHHCGVGAIOSSSTVDHYLRDGFVSRITMG-EELPIEGLSVKYLKRIIVKVTIDKRVGQLKGITD-
	P2	67	GGCTGEVVSQGLVVTNHHCGVDMIOAHSTLEHNYLENGFWAMREA-DELPNKDISVFLDKLEEDVIDVYKKDKAIKDKP
	S1	157	-----REFYQGVNQEKALVAECENKDEGYRCQVSYFHGGLEYMYLVKQLETRDVRVLYVNPAGSVGKVGCGVDNMMWPRHT
	S2	140	-----LKRYEIEIENHSAIKKSCFADENYRCNVRSFHNGLVYLIKQIMRDVRLVYAPPESSVGKVGCGVDNMMWPRHT
	X	146	-----PFKRITALETFSSKOEIAKCEPEQGYRCQVFFSAGGNIVRVFKNLEIKDVRVLYVAPQSSVGKVGCGVDNMMWPRHT
	P1	149	-----EMERLRKAQEVCOELAKKENADENQICIVPEFYSNNEVFLIVDYDFKDVNMVFAFPSSVGKVGCGVDNMMWPRHT
	P2	146	NSMDYLSPKYLQKLADKAGKNFSKNNPGLSVELKAFYGGNLYLMFTKKTYTQVRLVAGAPPTSTIGKFGADIDNMMWPRHT
	S1	231	GDYSFYRAYVSKNGKPAEFSADNVVPEPKSFLKVSAGVSEGDFFVMVAGYPGRTNRYRTATEVQNEFEMAYPEGKMLRER
	S2	214	GDFAFLRAYVGKDGKPAEFSADNVVPEPKSFLKVNADGVKAGDGVFVAGYPGRTNRYNLTSELKFSADMLYPTQAKRYQL
	X	221	GDFSFYRAYVGKDGKPAEFSADNVVPEPKSFLKVNADGVKAGDGVFVAGYPGRTNRYNLTSELKFSADMLYPTQAKRYQL
	P1	224	GDFSFYRAYVAGADNRPAEYSKDNKPYKPYVFAAVSMOQYKADPYAMTIGFPGSHDRYLISWGVEDRTEENENNPRIEVRGI
	P2	226	GDFSIFRIYADKNGNPAPYSEDNVPLKPKREFNLSLGGVQENDYAMTMGFPGITHRYFTASEVDEWKSIDNDIRIRMRDI
	S1	311	FTEITIKATAPEGSDEITKYVESQTAGLANVAKNFTSMTEFYGKSTMLADRKALFAKLAEMTAKDSS---REAKYGKTLAEL
	S2	294	QIDTHEAMGQKADIAIKYAGNMASMANRMKLANGLLAGFKATDIVGIKQORENDFLAWLIKPN-----LNQNLISEL
	X	301	LIALIEAASKQNPDIQVKYASTLAGLNNTSKNFDGQDGFRRINAIQKQSEETAVLAWLKQOGI---RGHEALAAHQTL
	P1	304	KQGWKEAMSADQATRIKAYASKYASQASANYMKNISGMNRGLARLDVIGKRAEERAFADWIKRCKSAV---YGDVLSLE
	P2	306	RQGVMLREMLADPQIKIMYSKAYASQASANYMKNISGMNRGLARLDVIGKRAEERAFADWIKRCKSAV---YGDVLSLE

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Fig. 6b

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Fig. 6b



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S1	388	DALIAKSKAHQERDMILSYISSITIMPTANNMLYRLAHEKQLPEMORPECFQDRMTFRFKASMERIDRRYAAASVDKAVLFD
S2	368	EVLLAEQOLOTQTNVYFTNAQSSILLTAANNLYRLAKKQKSDAEREIGYQERDLAMFSSRLKRIDSFFDVKKVILWLQ
X	378	VDLTEQYKANQDRDEVLGQFNCSGVIGVAVNLVRLAHERTKSDAQREAGYQERDLPTIEGNLKQMERRYLPEMTRQMOQY
P1	381	KAYKEGAKANRENTYLSSETLFGCTEIVVRFQAFANALATNPDAHAGILKSLDKYKDYLPDLDRKVLPAMLDIVRRRIIPAD
P2	380	IDATVAKRADLRRLRYMMIEEGIRGIEFFARSPIPTEDETKALQCNDA SARKEAIDKIRTRYSKFANKDYSAEVDKVAVA
S1	468	MLKRYAALPEAQRLPAMEKAFGIDNKNVNEAKLAKTEIDKMYAKTELGKQVRLAMKESVDDEKASKDPFTIQFAVAMVDTN
S2	448	DAN--AYLSQPNRVAALDNMNLNDKN--VSLAAKLDGLYSITITLTDQAQRIAMNEADAKARETSSDPTIRLAVALYDTN
X	458	MLTEYNKLPVKQRVAALDVWLGIGIPAT-----L-KRLGDTKLSSSEERLKWFNADRAAFESSQDPATIRYAVATMPAL
P1	461	KLPDIFKINVIDKKFKGDTTKYADFVD--KS-----VVPYSDKFHAMLKSMDEKFAKAEKDPAVELSKSVIAAA
P2	460	MLTEYMLKEIPYENLPLHLRLVKDRFAG---DVOAYVDDIFARSVFGSEAQQFDFAFAVPSVEKLAEDPMVLFASSVFDEY
S1	548	MSEERKEKELDGLMKVRPOYMDALIANNLEQEKPVYADANSLSRVITVGHVKGYSPKDGILVAVPFFTRLEGTVQKDTG-ID
S2	524	MAQEKAEKILACKLSTARPAYMAAVDYKANNMVPYDPANGTIRISYGMWDGYQSRDALYKQPTFRLDGLVAKHTG-VE
X	530	LEITERONKIRTGELTKARPIYLQALADYKSHGKFEVYDPANGSLRIHFECHVKGYSPKDGMEYTPFTTLOQGVMAKNITG-VE
P1	530	RAIQADAMANAYAEKGRLEFFAGIREMYP--CEALPSDANFTMRMSYCSITKGYEPQDCAMNYHTTCKGVTEKQDPKSD
P2	536	RKLYNELRPYDDPLLRQAORTYTAGLEEMDG--DQDQFPDANILFRFTYGOVKGYSPRDNVYVYGHQTTLTLDGVMEKEEDPDNW
S1	627	PFDAPKQOQLELIKQKQYGDFFYMKSIDS-----VPVNFSLSTLDTTGGNSGSPITENGRAELVGLIF
S2	603	PYNAPKKLIDATSVQRFQDHLVKSVYQDPRGWICRLFSCLDKPEEFNSVPVNFLLSSVDTTGGNSGSPVFNKGCELVGLNF
X	609	PFDSPKSLINATRAKSYANLADQRIGT-----VPVNFSLSDLDITGGNSGSPVLDAHGKLVGLAF
P1	608	EFVQVQNTIIDLFRITKNGYGRVAENGQLH-----IAF--LSNNDITGGNSGSPVFDKNGRLITGLAF
P2	614	EFVVDPKLKAHYERKDFGRYADRGRMP-----VAFCAITHTTGGNSGSPVMNANGELIGENF
S1	686	DGVYESITGGWAFDNEINRSIHVDSRYMLWVWKYLDHADNLLAEMETVN--
S2	683	DSITYEALTKDWFFNPTITRAVHVDIRYLLWMDVVDHADNLLKELDLVRN
X	668	DGNWESVSSNWVFDPMIRTIADVSRVQVINTENAPAPHLLKELNLYR-
P1	665	DGNWEAMSGDIEEFEDLORTISVDIRYVLFMDKW-----
P2	672	DRNWEVGGDIQYLADYQRSIIVDIRYVLLVIDKNGGCQRLDENMVP-

Fig. 6a